

APPROVED	O.G. FIG.
BY	CLASS SUBCLASS
DRAFTSMAN	

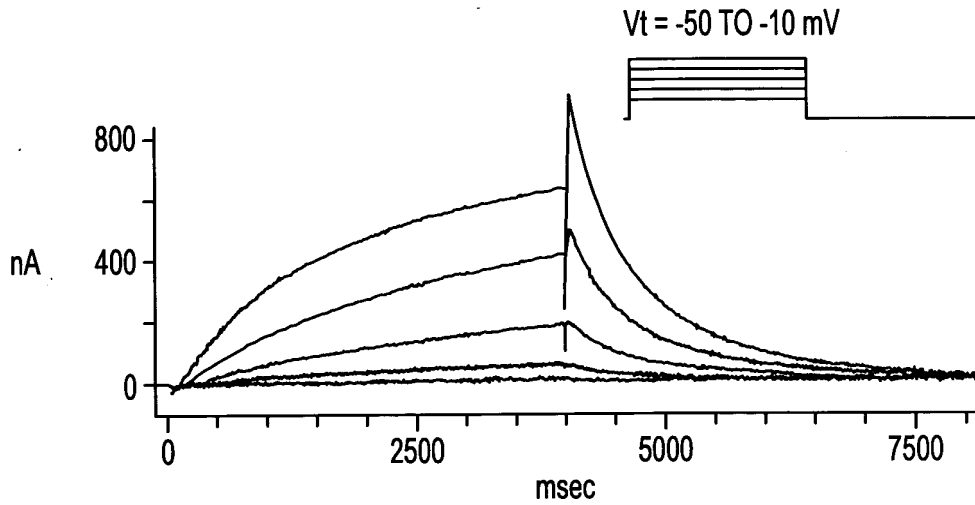


FIG. 1A

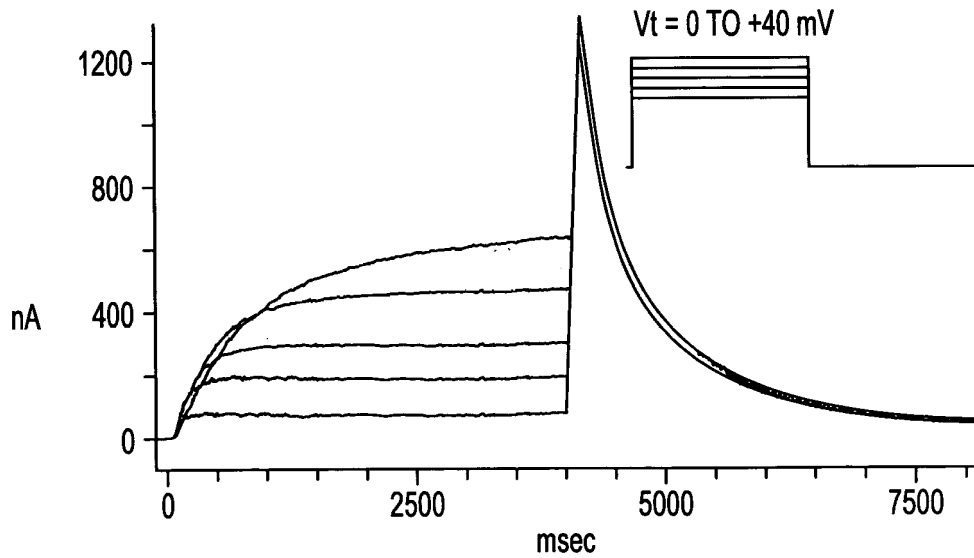


FIG. 1B

APPROVED	O.G. FIG.	
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001121 5665260

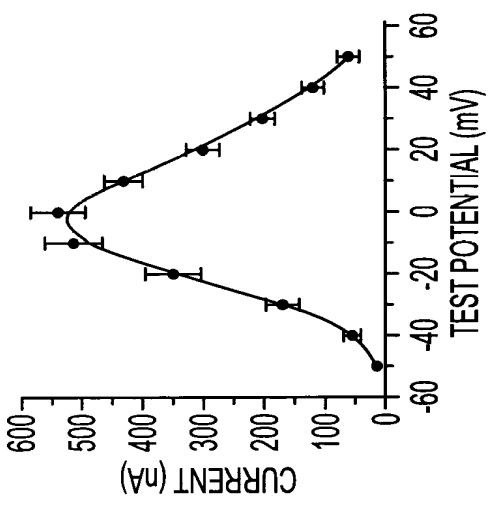


FIG. 1C

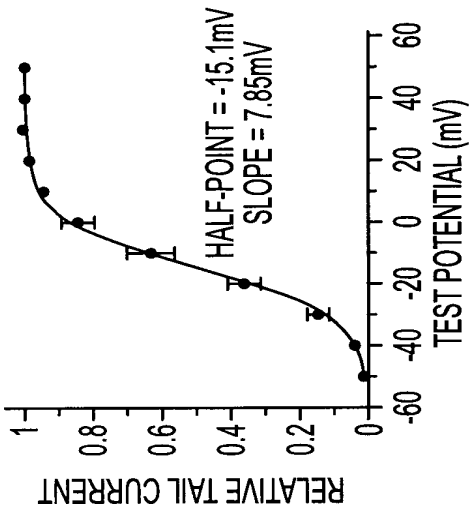


FIG. 1D

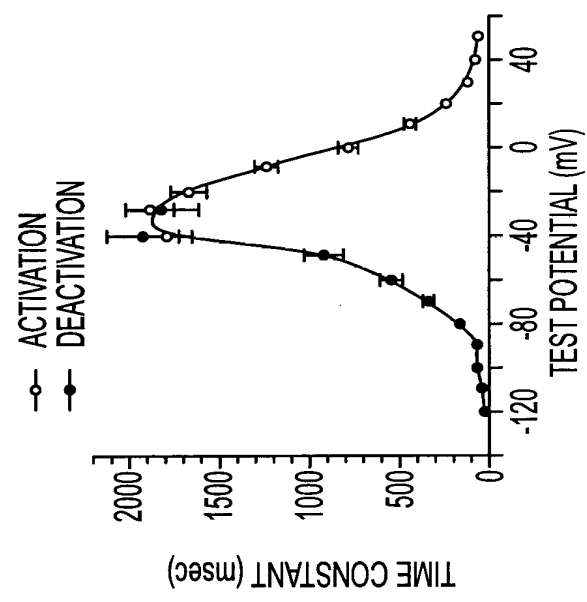


FIG. 2C

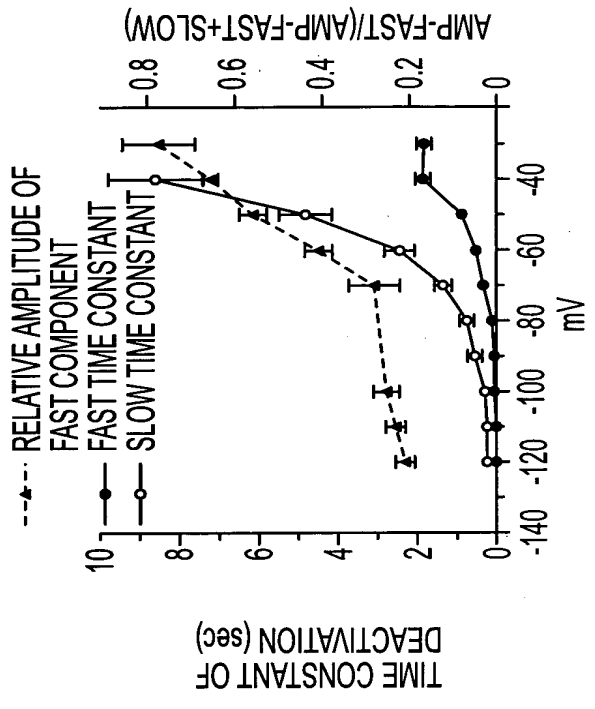


FIG. 2D

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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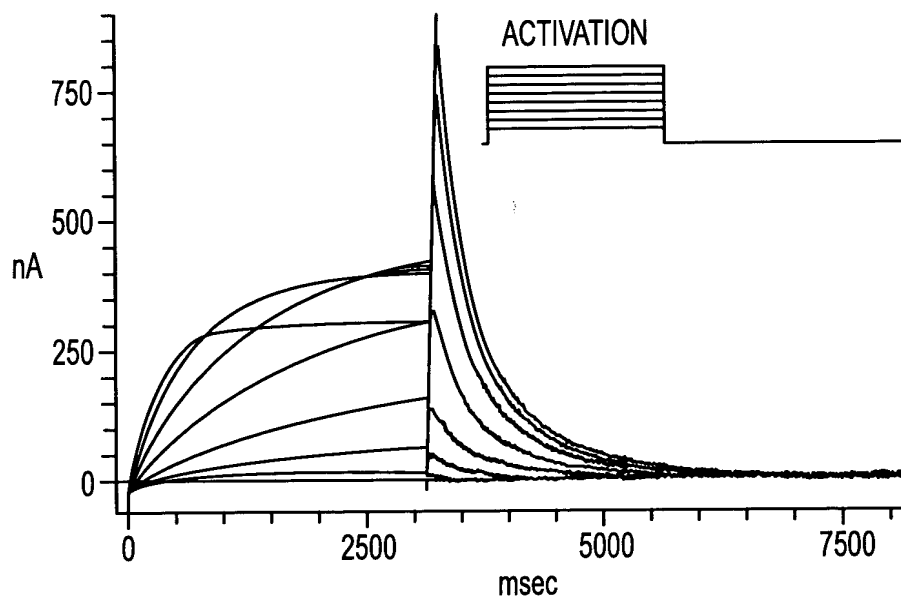


FIG. 2A

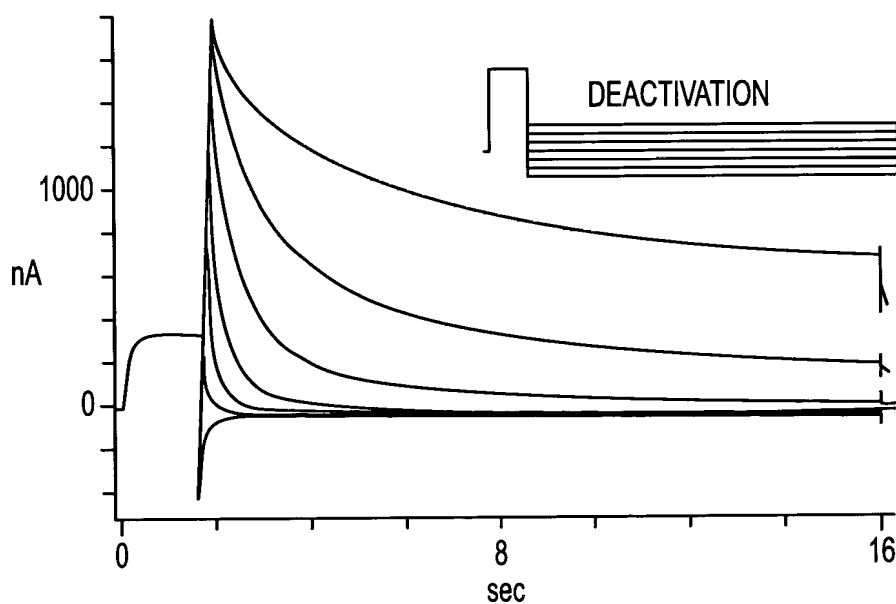


FIG. 2B

00735995-24400

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

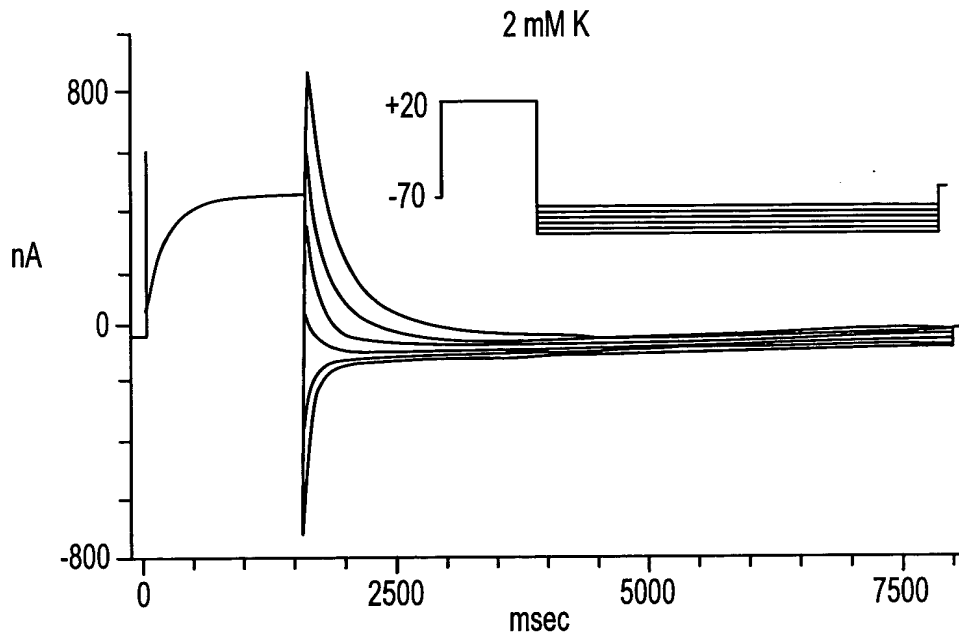


FIG. 3A

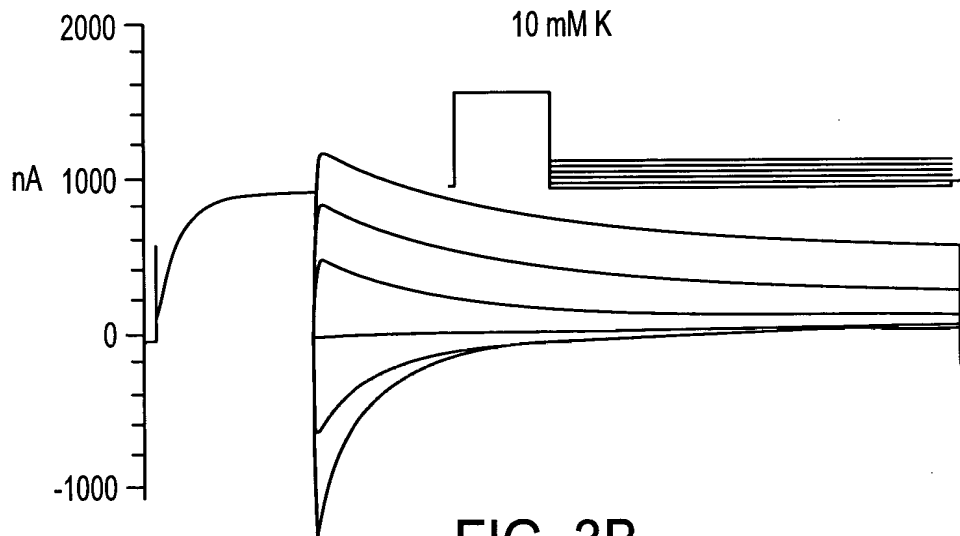


FIG. 3B

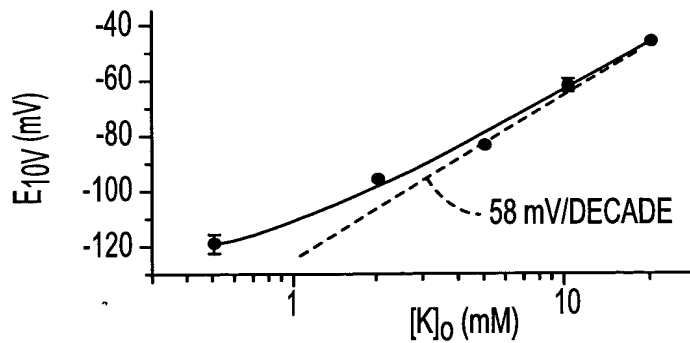


FIG. 3C

004727 56656460

APPROVED	O.G. FIG.	
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DRAFTSMAN		

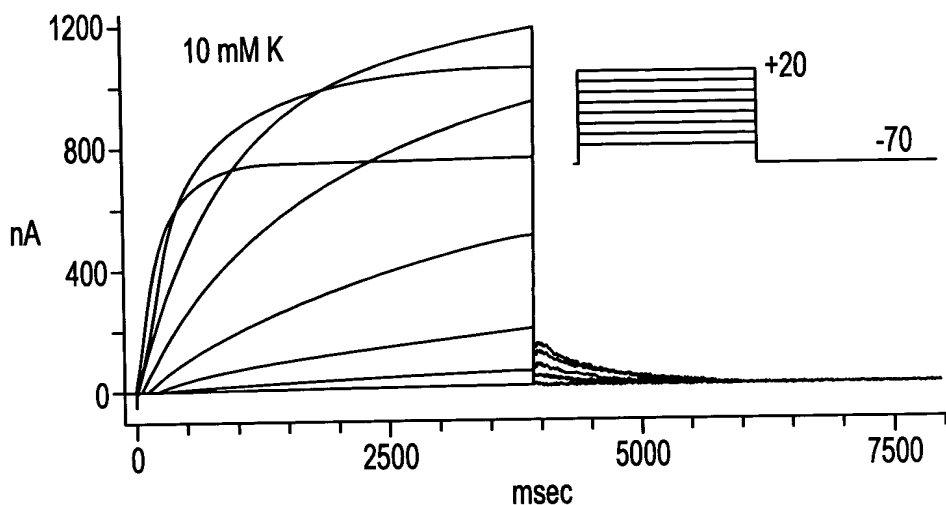


FIG. 4A

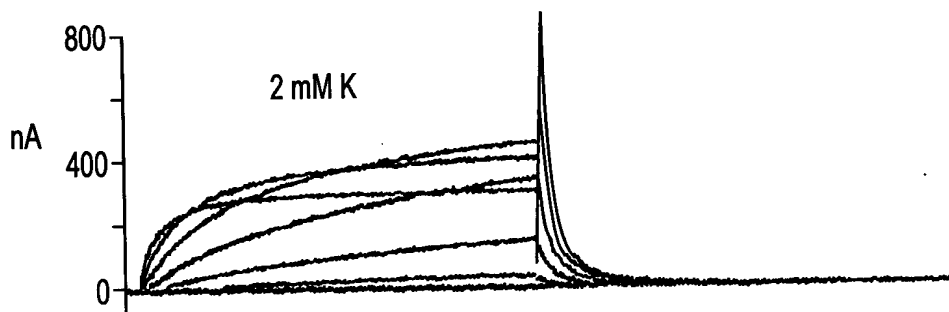


FIG. 4B

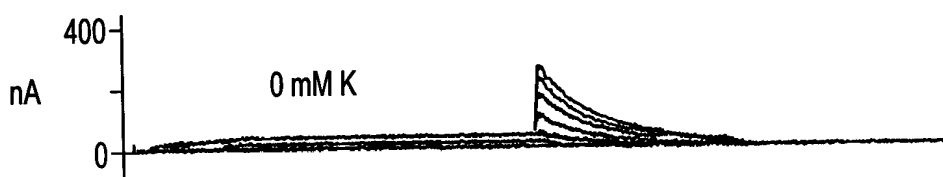


FIG. 4C

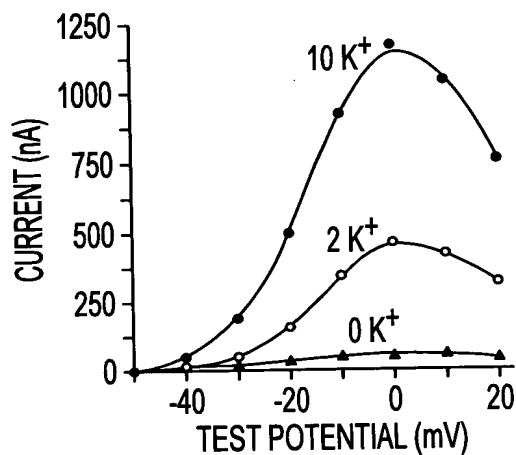


FIG. 4D

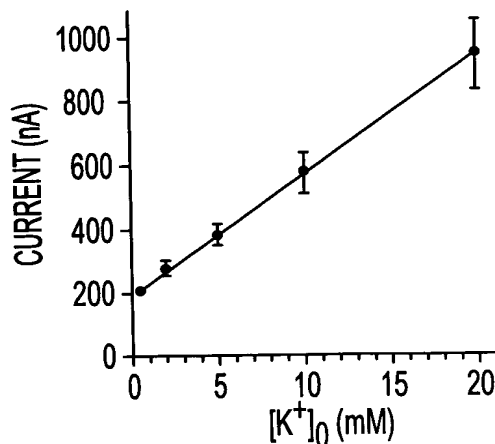


FIG. 4E

004727-5665260

APPROVED	O.G. FIG.	
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000000-5065E260

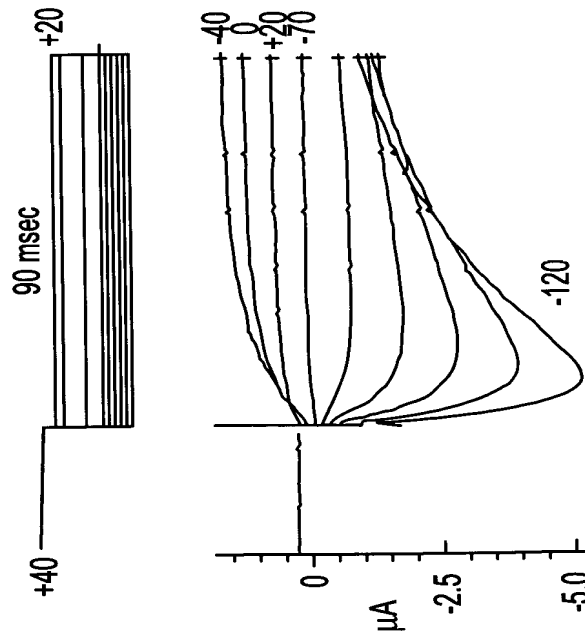


FIG. 5A

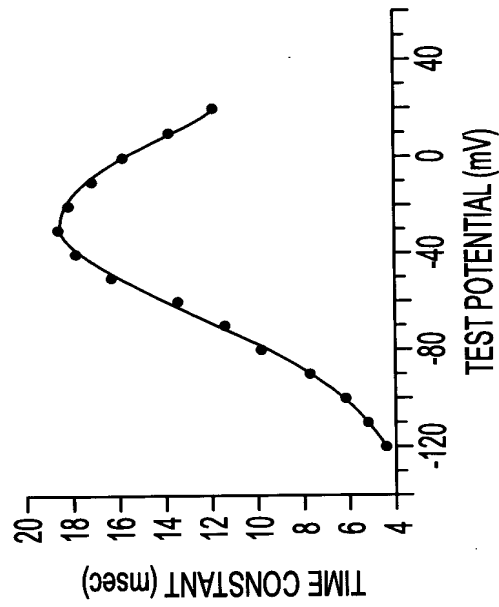


FIG. 5B



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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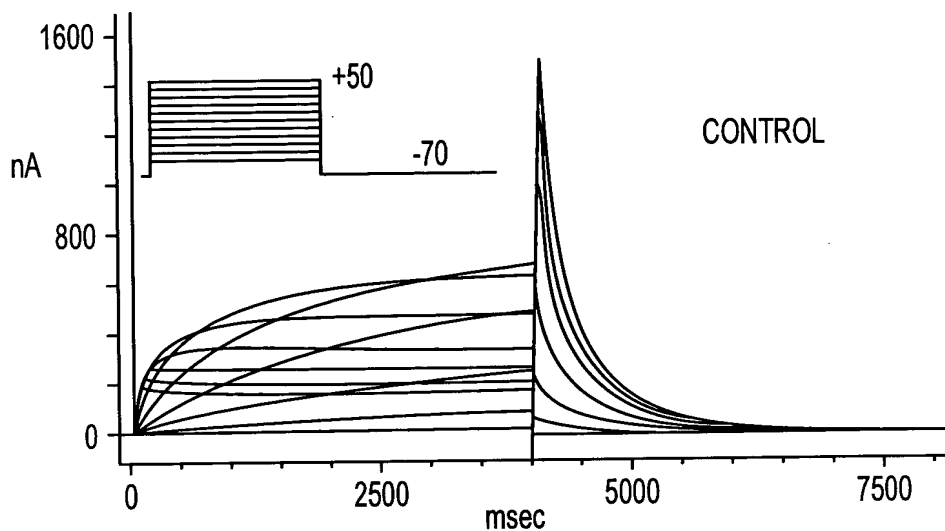


FIG. 6A

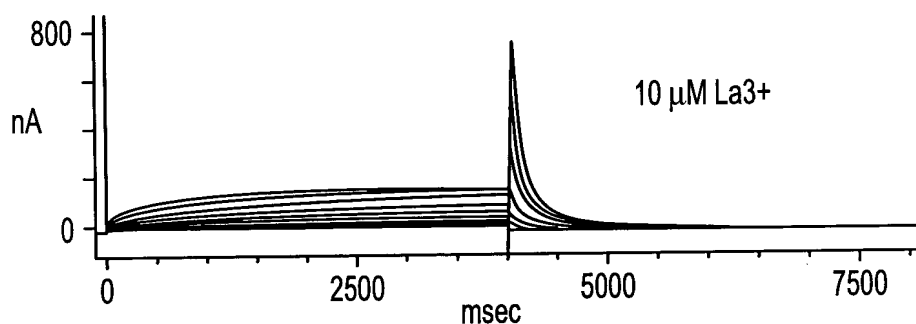


FIG. 6B

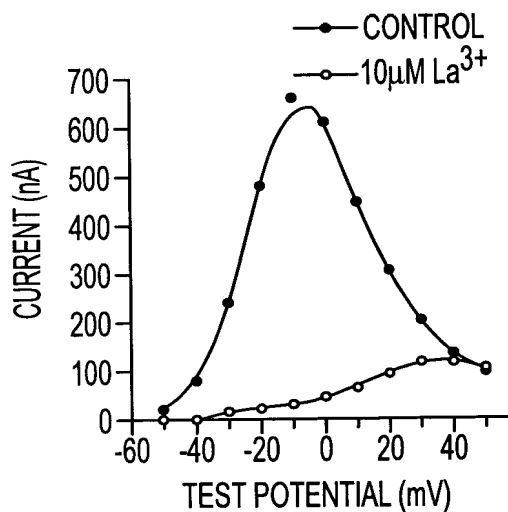


FIG. 6C

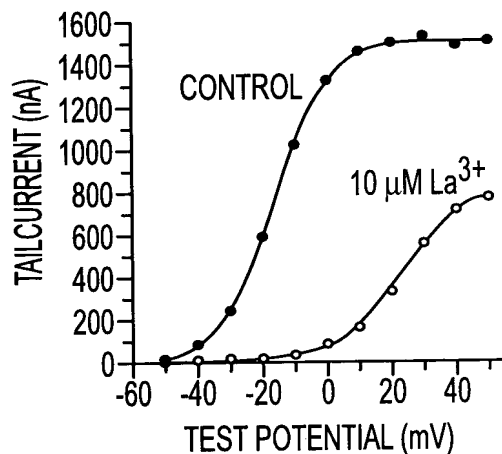


FIG. 6D

00735055 1440  
00735055 5055260



APPROVED	O.G. FIG.	
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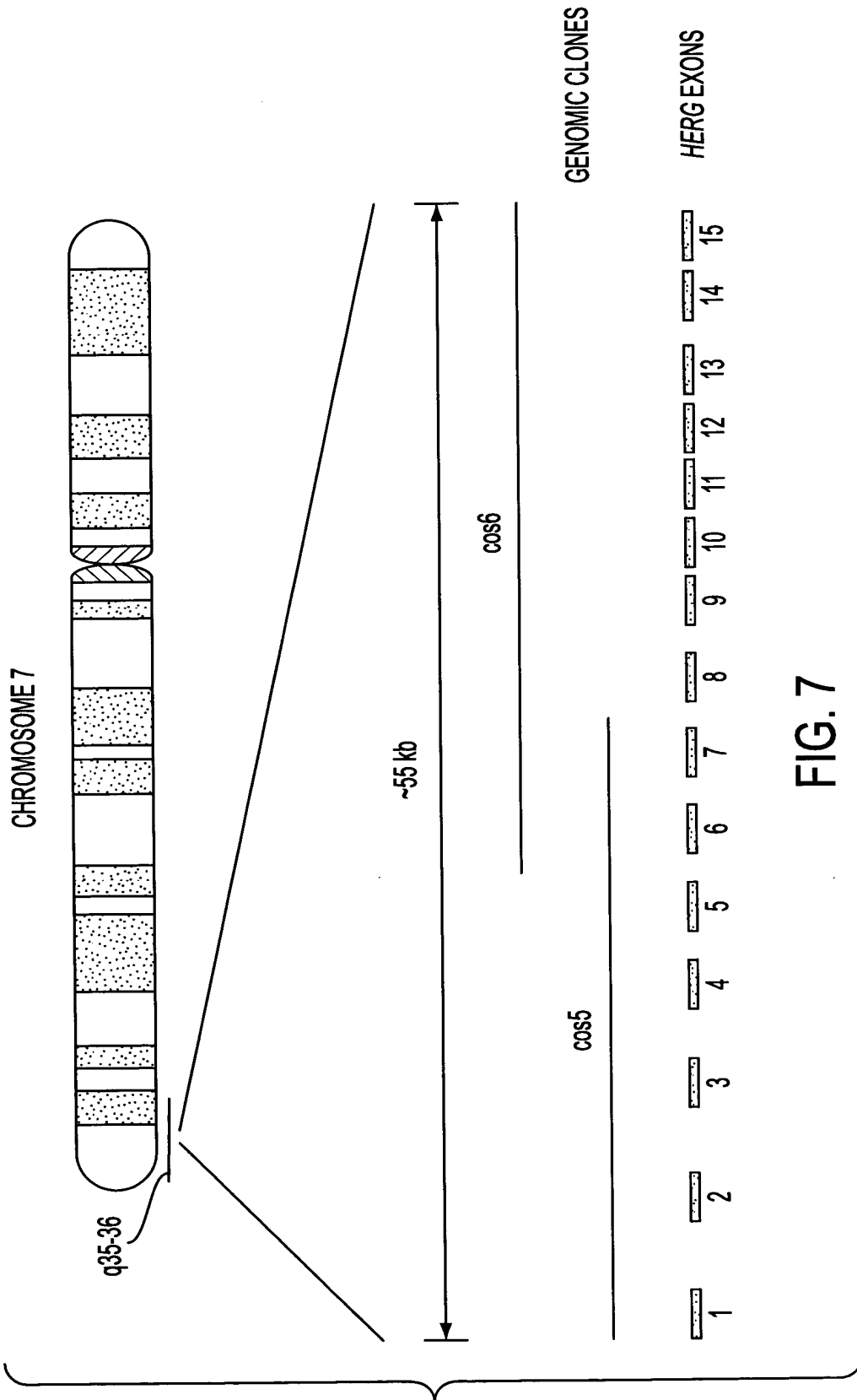


FIG. 7

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Mutations in and Genomic Structure  
of HERG - A Long QT Syndrome Gene  
Mark T. KEATING et al.  
Docket No.: 2323-156

09735056:24160

AGCCTAGTGCTGGGCCGGGCCGGGGTGGGTGGGGCCCGCCCGCCCATGGGCTCAGGATGCCGGTGCGGAGG-81  
GGCCACGTGCGCCGAGAACACCTTCTGGACACCATCATCCGCAAGTTTGAGGGCCAGAGCCGTAAGTTCATCATCGCC-162  
G H V A P Q N T F L D T I I R K F E G Q S R K F I I A -32  
AACGCTCGGGTGGAGAACTGCGCCGTCTACTGCAACGACGGCTTCTGCGAGCTGTGCGGCTACTCGCGGGCCGAGGTG-243  
N A R V E N C A V I Y C N D G F C E L C G Y S R A E V -59  
ATGCAGCGACCTGCACCTGCGACTTCCTGCACGGCCGCGCACGACGCCGCGCTGCCGCGCAGATCGCGCAGGCACTG-324  
M Q R P C T C D F L H G P R T Q R R A A A Q I A Q A L -86  
CTGGGCGCCGAGGAGCGCAAAGTGGAATCGCCTTCTACCGAAAGATGGGAGCTGCTTCTATGTCTGGTGGATGTGGTG-405  
L G A E E R K V E I A F Y R K D G S C F L C L V D V V -113  
CCCGTGAAGAACGAGGATGGGGCTGTCTATCATGTTTCATCCTCAATTTGAGGTGGTGGTGGAGAAGGACATGGTGGGGTCC-486  
P V K N E D G A V I M F I L N F E V V M E K D M V G S -140  
CCGGCTCATGACACCAACCACCGGGGCCCCCACCAGCTGGCTGGCCCCAGGCCGCGCAAGACCTTCCGCTGAAGCTG-567  
P A H D T N H R G P P T S W L A P G R A K T F R L K L -167  
CCCGCGTGTGGCGTACGGCCCGGAGTCGTCGGTGGGTGGGGCGCGGGCGCGGGCGCCCGGGGGCCGTG-648  
P A L L A L T A R E S S V R S G G A G G A G A P G A V -194  
GTGGTGGACGTGGACCTGACGCGCGGGCACCAGCAGCGAGTCGCTGGCCCTGGACGAAGTGACAGCCATGGACAACCAC-729  
V V D V D L T P A A P S S E S L A L D E V T A M D N H -221  
GTGGCAGGGCTCGGGCCCGGAGGAGCGCGTGGCTGGGTCCCGGCTCTCCGCCCGCAGCGCGCCGGCCAGCTC-810  
V A G L G P A E E R R A L V G P G S P P R S A P G Q L -248  
CCATCGCCCCGGGCGCACAGCCTCAACCCGACGCTCGGGCTCCAGCTGCAGCCTGGCCCGGACGCGCTCCCGAGAAAGC-891  
P S P R A H S L N P D A S G S S C S L A R T R S R E S -275  
TGCGCCAGCGTGCGCCGCGCTCGTCGGCCGACGACATCGAGGCCATGCGCGCGGGGTGCTGCCCCCGCCACCGCGCCAC-972  
C A S V R R A S S A D D I E A M R A G V L P P P P R H -302  
GCCAGCACCGGGCCATGCACCCACTGCGCAGCGGCTTGCTCAACTCCACCTCGGACTCCGACCTCGTGGCTACCGCACC-1053  
A S T G A M H P L R S G L L N S T S D S D L V R Y R T -329  
ATTAGCAAGATTCCCCAAATCACCTCAACTTTGTGGACCTCAAGGGCAGCCCTTCTTGGCTTCGCCACCACTGACCGT-1134  
I S K I P Q I T L N F V D L K G D P F L A S P T S D R -356  
GAGATCATAGCACCTAAGATAAAGGAGCGAACCACAATGTCACTGAGAAGGTCACCCAGGTCCTGTCCCTGGGCGCCGAC-1215  
E I I A P K I K E R T H N V T E K V T Q V L S L G A D -383  
GTGCTGCCTGAGTACAAGCTGCAGGCACCGCATCCACCGCTGGACCATCTGCATTACAGCCCCCTTAAGGCCGTGTGG-1296  
V L P E Y K L Q A P R I H R W T I L H Y S P F K A V W -410  
GACTGGCTCATCTGTCTGGTTCATCTACACGGCTGTCTTACACCCCTACTCGGCTGCCTTCTGCTGAAGGAGACGGAA-1377  
D W L I L L L V I Y T A V F T P Y S A A F L L K E T E -437  
S1  
GAAGCCCGCCTGCTACCGAGTGTGGCTACGCTGCCAGCCGCTGGCTGTGGTGGACCTCATCGTGGACATCATGTTTCATT-1458  
E G P P A T E C G Y A C Q P L A V V D L I V D I M F I -464  
S2  
GTGGACATCCTCATCAACTTCCGCACCACCTACGTCAATGCCAACGAGGAGGTGGTCAGCCACCCCGCCGATCGCCGTC-1539  
V D I L I N F R T T Y V N A N E E V V S H P G R I A V -491  
CACTACTTCAAGGGCTGGTTCCTCATCGACATGGTGGCCGCCATCCCTTCGACCTGCTCATCTTCGGCTCTGGCTCTGAG-1620  
H Y F K G W F L I D M V A A I P F D L L I F G S G S E -518  
S3  
GAGCTGATCGGGCTGCTGAAGACTGCGCGGCTGCTGCGGCTGGTGGCGGGAAGCTGGATCGCTACTCAGAGTAC-1701  
E L I G L L K T A R L L R L V R V A R K L D R Y S E Y -545  
S4  
GGCGCGCCGCTGCTGTTCTTGTCTCATGTGCACCTTTGCGCTCATCGCGCACTGGCTAGCCTGCATCTGGTACGCCATCGGC-1782  
G A A V L F L L M C T F A L I A H W L A C I W Y A I G -572  
S5  
AACATGGAGCAGCCACACATGGACTCAGCATCGGCTGGCTGCACAACCTGGGCGACAGATAGGCAAACCTACAACAGC-1863  
N M E O P H M D S R I G W L H N L G D O I G K P Y N S -599  
AGCGGCTGGGCGGCCCTCCATCAAGGACAAGTATGTGACGGCGCTCTACTTACCTTACAGCAGCTCACCAGTGTGGGC-1944  
S G L G G P S I K D K Y V T A L Y F T F S S L T S V G -626  
Pore  
TTCGGCAACGTCTCTCCCAACCAACTCAGAGAAGATCTTCTCCATCTGCGTCATGCTATTGGCTCCCTCATGTATGCT-2025  
F G N V S P N T N S E K I F S I C V M L I G S L M Y A -653  
S6

FIG. 8A

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

AGCATCTTCGGCAACGTGTCGCCATCATCCAGCGGCTGTACTCGGGCACAGCCCGCTACCACACACAGATGCTGCGGGTG-2106  
S I F G N V S A I I O R L Y S G T A R Y H T Q M L R V -680

CGGGAGTTCATCCGCTTCCACCAGATCCCCAATCCCTGCGCCAGCGCCTCGAGGAGTACTTCCAGCAGCCTGGTCTCTAC-2187  
R E F I R F H Q I P N P L R Q R L E E Y F Q H A W S Y -707

▽

ACCAACGGCATCGACATGAACGCGGTGCTGAAGGGCTTCCCTGAGTGCCTGCAGGCTGACATCTGCCTGCACCTGAACCGC-2268  
T N G I D M N A V L K G F P E C L Q A D I C L H L N R -734  
TCACTGCTGCAGCACTGCAAACCTTCCGAGGGGCCACCAAGGGCTGCCTTCGGGCCCTGGCCATGAAGTTCAAGACCACA-2349  
S L L Q H C K P F R G A T K G C L R A L A M K F K T T -761  
CATGCACCGCCAGGGACACACTGGTGCATGCTGGGACCTGCTCACCGCCCTGTACTTCATCTCCCGGGGCTCCATCGAG-2430  
H A P P G D T L V H A G D L L T A L Y F I S R G S I E -788

▽

ATCCTGCGGGGCGACGTCGTCGTGGCCATCCTGGGGAAGAATGACATCTTTGGGGAGCCTCTGAACCTGTATGCAAGGCCT-2511  
I L R G D V V V A I L G K N D I F G E P L N L Y A R P -815

CNBD

GGCAAGTCGAACGGGGATGTGCGGGCCCTCACCTACTGTGACCTACACAAGATCCATCGGGACGACCTGCTGGAGGTGCTG-2592  
G K S N G D V R A L T Y C D L H K I H R D D L L E V L -842

▽

GACATGTACCTGAGTTCTCCGACCACTTCTGGTCCAGCCTGGAGATCACCTTCAACCTGCGAGATACCAACATGATCCCG-2673  
D M Y P E F S D H F W S S L E I T F N L R D T N M I P -869  
GGCTCCCCCGGAGTACGGAGTTAGAGGGTGGCTTCAGTCGGCAACGCAAGCGCAAGTTGTCTTCCGAGCGGCACGGAC-2754  
G S P G S T E L E G G F S R Q R K R K L S F R R R T D -896

▽

AAGGACACGGAGCAGCCAGGGAGGTGTGCGCCTTGGGGCCGGGCGGGCGGGGCGAGGCGCGAGTAGCCGGGGCCGGCCG-2835  
K D T E Q P G E V S A L G P G R A G A G P S S R G R P -923  
GGGGGGCGTGGGGGAGAGCCCGTCCAGTGGCCCTCCAGCCCTGAGAGCAGTGAAGATGAGGGCCAGGCCGAGCTCC-2916  
G G P W G E S P S S G P S S P E S S E D E G P G R S S -950  
AGCCCCCTCCGCTGGTGCCTTCTCCAGCCCCAGGCCCCCGGAGAGCCGCGGGTGGGGAGCCCTGATGGAGGACTGC-2997  
S P L R L V P F S S P R P P G E P P G G E P L M E D C -977

▽

GAGAAGAGCAGCGACACTTGCAACCCCTGTGAGGCGCCTTCTCAGGAGTGTCCAACATTTTCAGCTTCTGGGGGGACAGT-3078  
E K S S D T C N P L S G A F S G V S N I F S F W G D S -1004  
CGGGGCCCGCAGTACCAGGAGCTCCCTCGATGCCCCGCCCCACCCCCAGCCTCTCAACATCCCCCTCTCCAGCCCCGGT-3159  
R G R Q Y Q E L P R C P A P T P S L L N I P L S S P G -1031

▽

CGGCGGCCCCGGGGCGACGTGGAGAGCAGGCTGGATGCCCTCCAGCGCCAGCTCAACAGGCTGGAGACCCGGCTGAGTGCA-3240  
R R P R G D V E S R L D A L Q R Q L N R L E T R L S A -1058  
GACATGGCCACTGTCTGCAGCTGCTACAGAGGAGATGACGCTGGTCCCGCCCGCTACAGTGTGTGACCACCCCGGG-3321  
D M A T V L Q L L Q R Q M T L V P P A Y S A V T T P G -1085

▽

CCTGGCCCCACTTCCACATCCCCGCTGTTGCCCGTCAGCCCCCTCCCCACCTCACCTTGGACTCGCTTCTCAGGTTTCC-3402  
P G P T S T S P L L P V S P L P T L T L D S L S Q V S -1112  
CAGTTCATGGCGTGTGAGGAGCTGCCCCGGGGCCCCAGAGCTTCCCCAAGAAGCCCCACACGACGCTCTCCCTACCG-3483  
Q F M A C E E L P P G A P E L P Q E G P T R R L S L P -1139  
GGCCAGCTGGGGGCCCCACCTCCCAGCCCCGTCACAGACACGGCTCGGACCCGGGCAGTTAGTGGGGCTGCCAGTGTGG-3564  
G Q L G A L T S Q P L H R H G S D P G S \* -1159  
ACACGTGGCTCACCCAGGATCAAGGCGTGCTGGGCGCTCCCTTGGAGGCCCTGCTCAGGAGGCCCTGACCGTGGAAG-3645  
GGGAGAGGAACTCGAAAGCAGCTCCTCCCCAGCCCTTGGGACCATCTTCTCCTGCAGTCCCCTGGGCCCCAGTGAGAG-3726  
GGGCAGGGGCGGGCCGAGTAGGTGGGCGCTGTGGTCCCCCACTGCCCTGAGGGCATTAGCTGGTCTAACTGCCCGGA-3807  
GGCAGCCGCCCCCTGGGCTTAGGCACCTCAAGGACTTTTCTGCTATTTACTGCTTATTGTTAAGGATAATAATTAAGGA-3888  
TCATATGAATAATTAATGAAGATGCTGATGACTATGAATAATAATAATTATCCTGAGGAG (A)<sub>n</sub> -3949

FIG. 8B

0047-5656/96

K1956

K2287

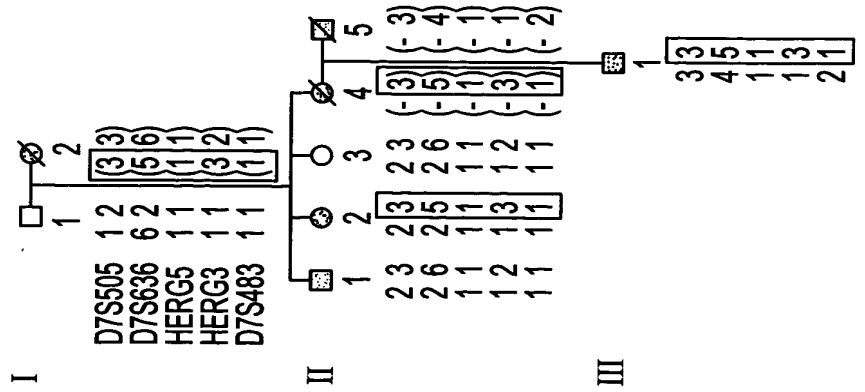


FIG. 9A

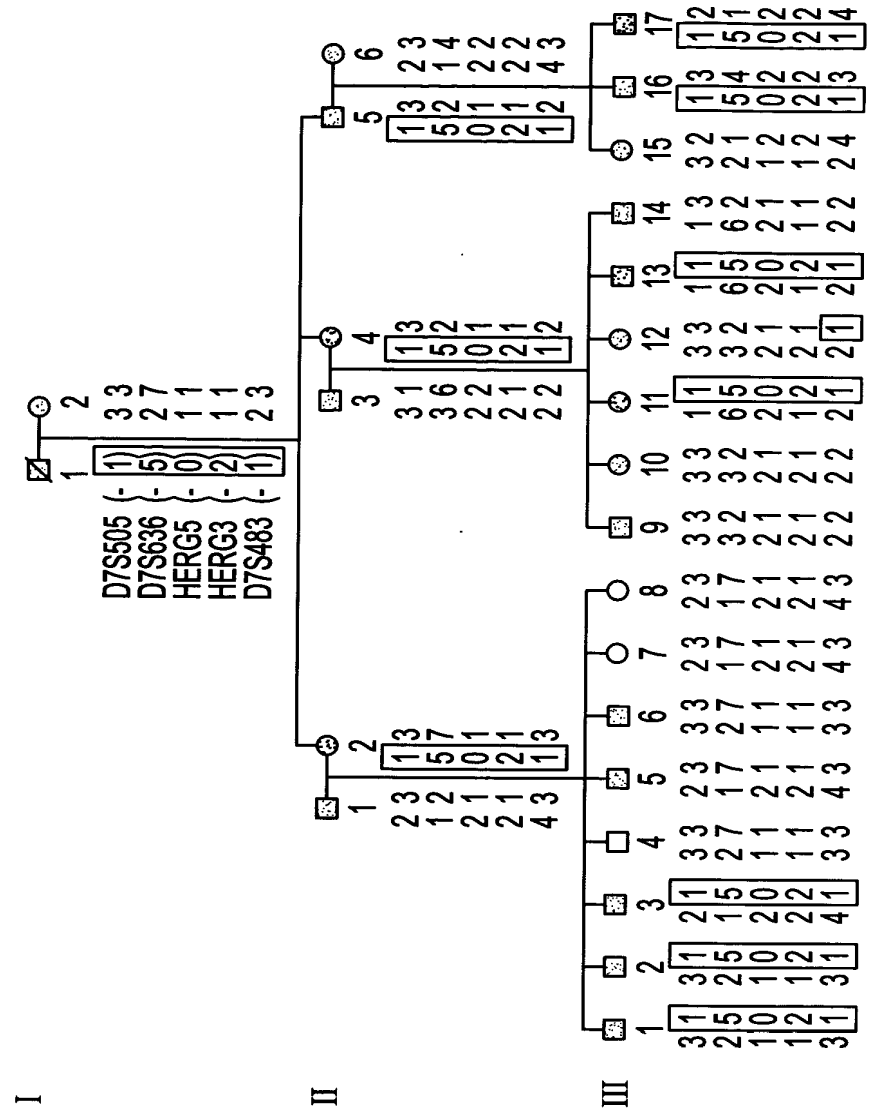
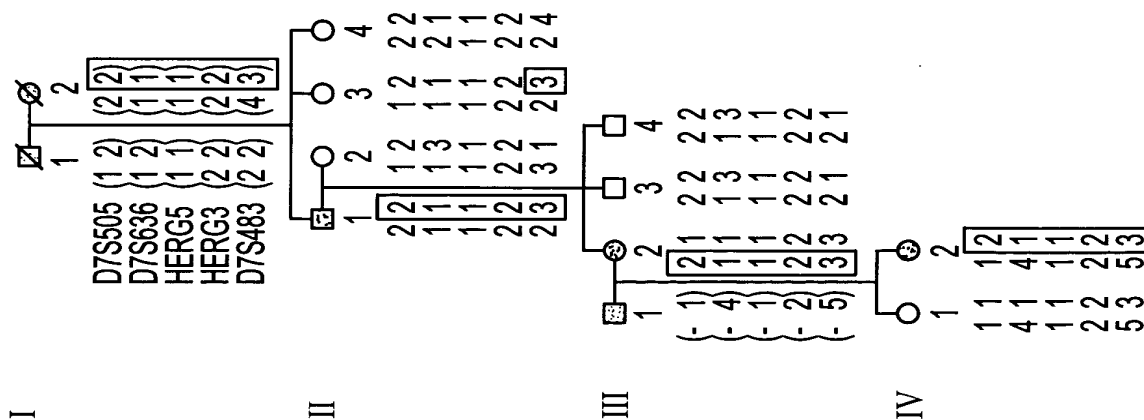


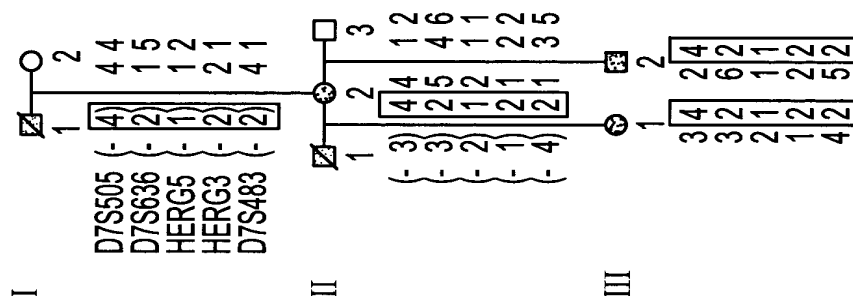
FIG. 9B

004121-5665260

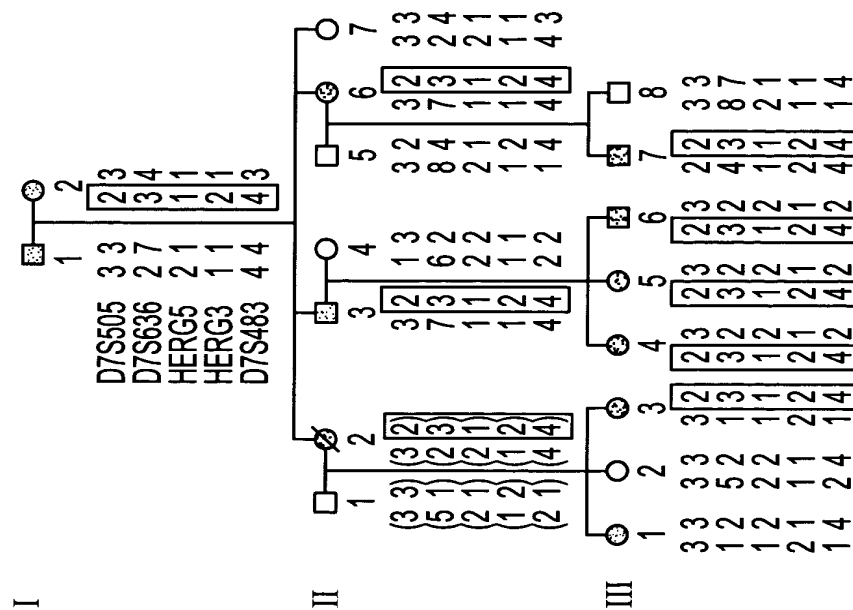
K2595



K2596



K2600



APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

000000-56656666

TGG TTC CTC ATC GAC ATG GTG GCC GCC ATC CCC TTC GAC CTG CTC SEQ ID NO:96  
W F L I D M V A A I P F D L L SEQ ID NO:97  
S3

FIG. 10C

NORMAL GTC ATC TAC ACG GCT GTC TTC ACA CCC TAC TCG GCT TTC CTG CTG AAG GAG SEQ ID NO:98  
V I Y T A V F T P Y S A A F L L K E SEQ ID NO:99

DELETION GTC ATC TAC CGG CTG TCT TCA CAC CCT ACT CGG CTG CCT TCC TGC TGA SEQ ID NO:100  
V I Y R L S S H P T R L P S C SEQ ID NO:101

FIG. 11C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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004427-56656260

	GTG → V GCG //	SEQ ID NO:
K1956	L I A H W L	102
H-Erg	L I V H W L	103
M-Eag	L I A H W L	104
R-Eag	L A A H W K	105
Eag	L A A H W M	106
Elk	L V A H W L	107
	L A A H W L	108

← S5 →

	GAC → D AAC //	SEQ ID NO:
K2596	D I L I N F R	109
H-Erg	D I L I D F R	108
M-Eag	D I L I N F R	110
R-Eag	D I V L N F H	110
Eag	D I V L N F H	110
Elk	D I V L N F H	111
	D I L I N F R	111

← S2 →

FIG. 12G

FIG. 12H

5'-CAT CCT GG // gtatggg-3'  
c ↓

FIG. 12I

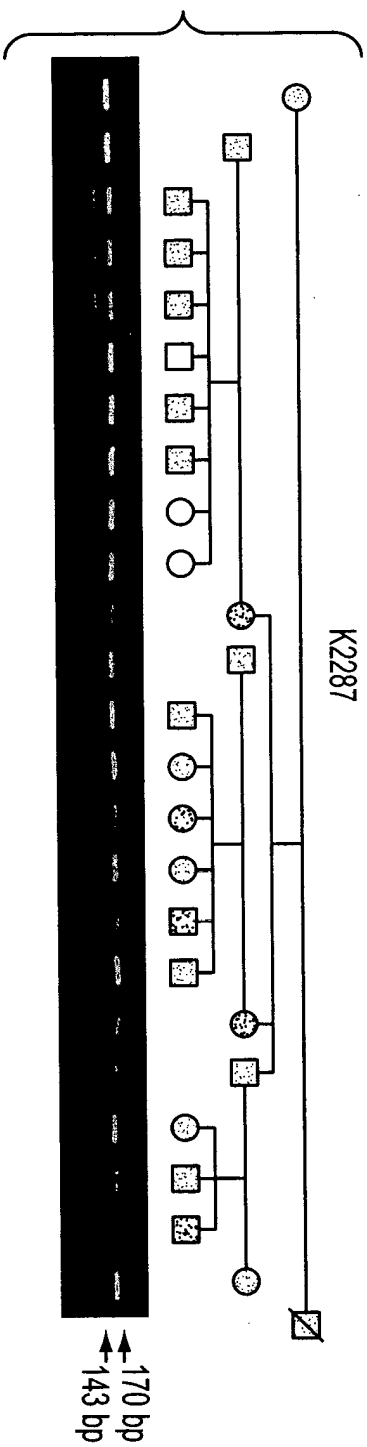


FIG. 10A

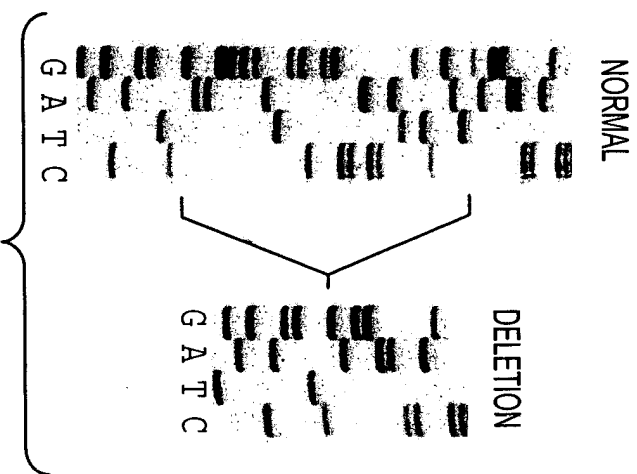


FIG. 10B



Docket No.: 2323-156

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BY \_\_\_\_\_  
DRAFTSMAN \_\_\_\_\_

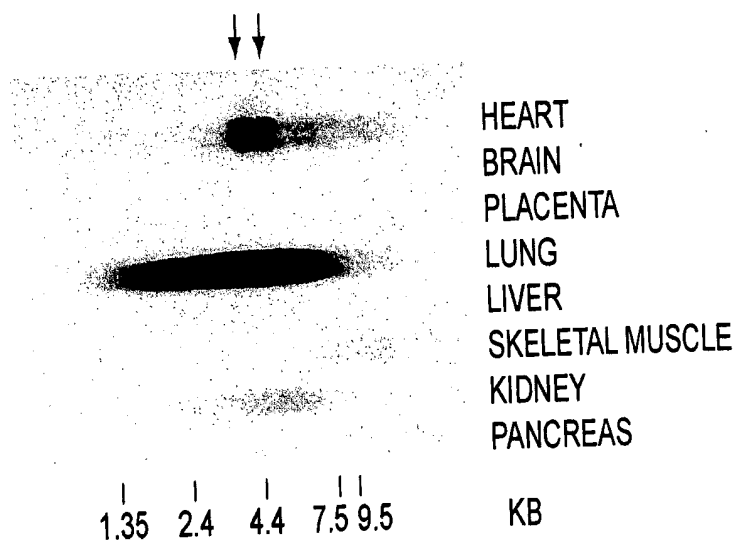


FIG. 15

APPROVED	C.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

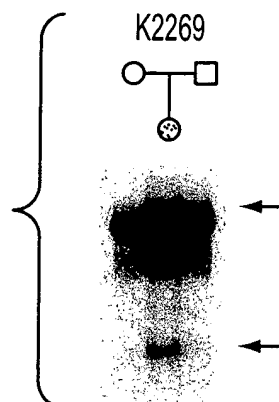


FIG. 14A

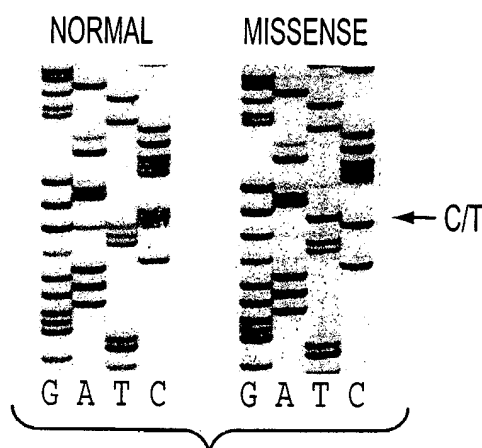


FIG. 14B

	AGC → S	SEQ ID
	GGC	NO:
	SVGFGNVS	112
	← PORE →	
K2269	SVGFSNVS	113
H-Erg	SVGFGNVS	112
M-Eag	SVGFGNIA	114
R-Eag	SVGFGNIA	114
Eag	SVGFGNVA	115
Elk	SVGFGNVS	112
Shaker	TVGYGDMT	116

FIG. 14C

0973595-14400

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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001421-5666260

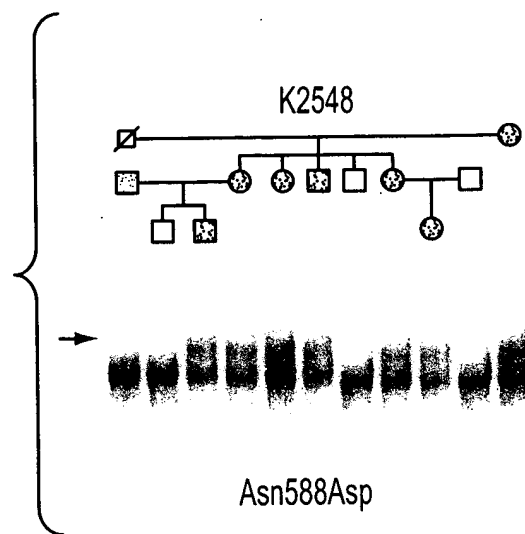


FIG. 13A



FIG. 13B

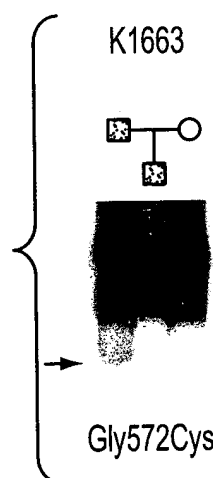


FIG. 13C

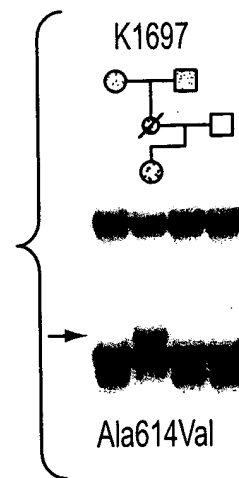


FIG. 13D

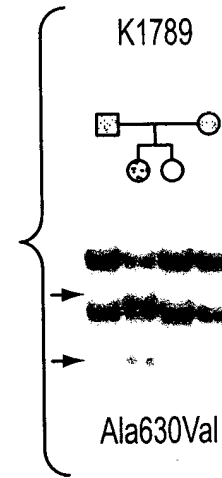


FIG. 13E

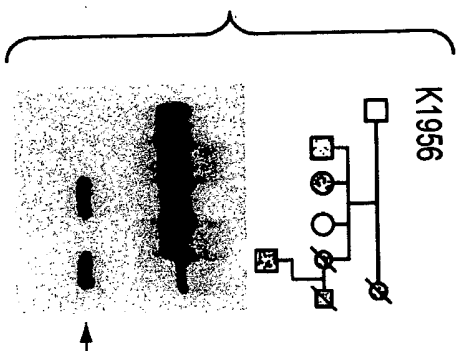


FIG. 12A

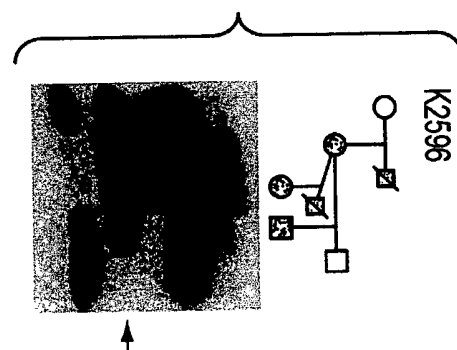


FIG. 12C

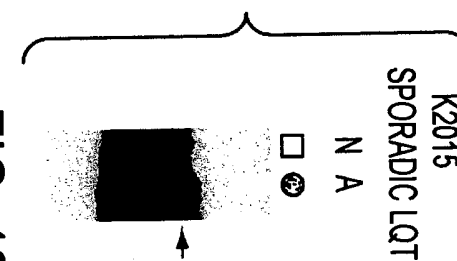


FIG. 12E

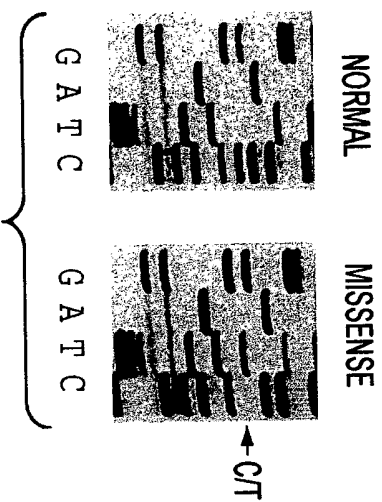


FIG. 12B

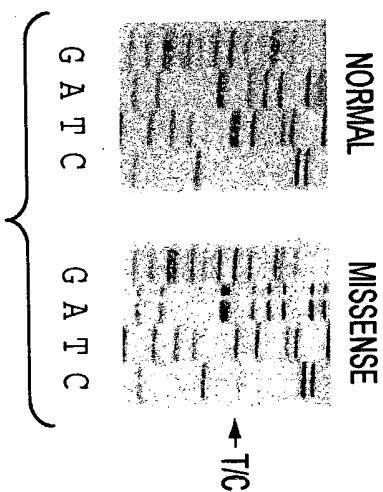


FIG. 12D

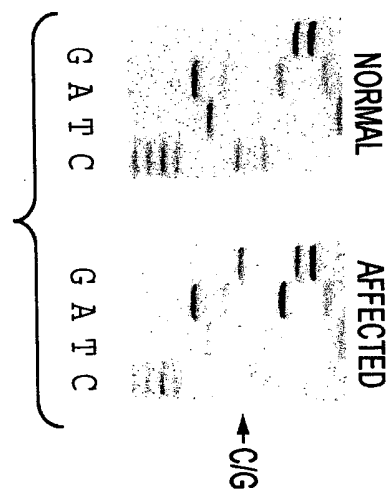


FIG. 12F

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

Mutations in and Genomic Structure  
of HERG - A Long QT Syndrome Gene  
Mark T. KEATING et al.  
Docket No.: 2323-156

00735995-10490

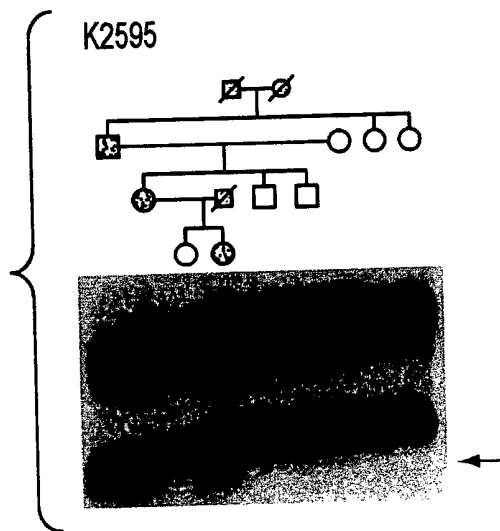


FIG. 11A

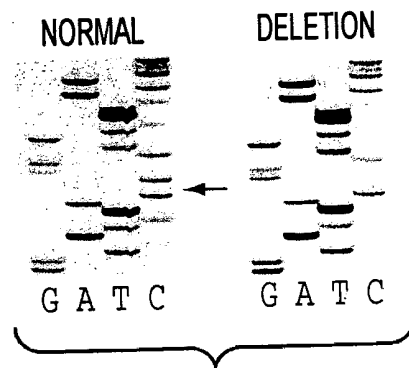


FIG. 11B